

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,409B

DATE: 06/25/2003 RECEIVED

SEP 2 2 2003 TECH CENTER 1600/2900

FITER

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Output Set: N:\CRF4\06252003\I804409B.raw

Input Set : A:\0278721.APP.txt

- 3 110 APPLICANT: ENGENE, INC. KIEFFER, TIMOTHY J.
- CHEUNG, ANTHONY T.
- 7 H120- TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
- EXPRESSION IN GUT
- 10 H130% FILE REFERENCE: 029996/027 8721
- 15 140 CURRENT APPLICATION NUMBER: 09/804,409B
- 13 -: 141 CURRENT FILING DATE: 2001-03-12
- 15 <160 NUMBER OF SEQ ID NOS: 19
- 17 -: 170 SOFTWARE: Fatentin Ver. 2.1
- 19 -010 SEO ID NO: 1
- 00 +0011 / LENGTH: 19
- L1 -0010 TYPE: DNA
- 77 +0213 + 05/GANISM: Artificial Sequence
- 14 -1100 FEATURE:
- 15 1213 OTHER INFORMATION: Description of Artificial Sequence: Primer
- 17 K4000 SEQUENCE: 1
- 18 bbadcogcag cottigtga
- 31 K210. SEQ ID NO: 2
- 32 <211 LENGTH: 21
- 33 K2125 TYPE: DNA
- 34 RO13> ORGANUSM: Artificial Sequence
- 36 <000> FEATURE:
- 57 x103 OTHER INFORMATION: Description of Artificial Sequence: Primer
- 39 <4000 SEQUENCE: 2
- 40 gytabagcat tyttocacaa tg
- 43 2100 SEQ ID NO: 3
- 44 1111 LENGTH: 19
- 45 01/0 TYPE: DNA
- 46 213 OFGANISM: Artificial Sequence
- 48 LLOU- FEATURE:
- 49 222 OTHER INFORMATION: Description of Artificial Sequence: Primer
- 51 R400% SEQUENCE: 3
- 57 addacdaged ctaamigat
- 55 <0100 SEQ ID NO: 4
- 50 -0110 LENGTH: 21
- 57 HOICH TYPE: DNA
- 58 HIII ORGANISM: Artificial Sequence
- 60 HLOOK FEATURE:
- el alleba OTHER INFORMATION: Description of Artificial Sequence: Primer
- 63 HIGHER SEQUENCE: 4
- £4 utaquitgoug taqticloca go
- 67 K2100 SEQ ID NO: 5

DATE: 06/25/2003 PATENT APPLICATION: US/09/804,409B TIME: 16:19:06

Input Set : A:\0278721.APP.txt

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68 - (211 > LENGTH: 1319
69 - 012 TYPE: DNA
70 <213 / ORGANISM: Mus musculus
7. 4400 > SEQUENCE: 5
75 degaaattad deactaegtt ggaattetat aagggttggg titgetgitt tigttadage 60
74 twoqtottig qoacceagoa bagotgaqtq qttotaagoo caeqtoqatq ottaacacat 120
75 quittattaaa taaatacaca ogaagooggi totoatittag gggoatgagi aggoagaggi 180
76 qtgggcagga agnaggaaag agoggaaaca ggtgoggaca gaaaggaggg gototgaagg 240
77 atgocagtea gtgccaaact gtcatccaga taccaggttc actgtggccc taggccagge 500
78 tgcaegggde ttoecatgtg gtetgeecag ggtgagagea gaactgeggt gggegggea 360
74 qaagqaaaco aaccaggaag cagggttgca cocaaattat ocaggtttta agtacattta 420\,
80 aqagacaaqg ctqqqctqtt qaaggtcaga ggtqtccctq gggtqctqqa ctaggactga 480
81 scaettetgt titagittaa tyytyägääs työeteacad tyetaeetyö ettäettyöe 540
82 oottgagago tgtgagoota ggacccacco atgtgtgggt tggaccttca gtcacacact 600
83 qaacqtgtqt qaaqccactq gttgtcagag cagggctctc ggcactgagg aagcagtgac 660
84 dactateche tateaaataa caattaaata cacacagaat gegaggeaca caactgagtt 720
85 toaggagagg octogotoag goaaggggtt caagaggett otgtggggaco ogotggatgt 780
86 topagggagt tottaaagat gggbytgbot beagebaagt gaaatbaaga gaaaagtabg 840
87 ogaagtatag gaasactcag cagtotggag aggtaaatag gggaggaatc cgaggotcag 900
88 agacaggagt gacttgccca oggacgcaca gcaagttggc aggtggagtt cagctgtgcc 960
89 acctitotgaa geogggiado ottitadagod accagatada agogggatag agadagotga 1020
90 tqqaqaaqot qqaqqtqqqq qqoqqqaooc cqaaqqtqqq qaaaqqqoqc qqqqqqqqq 1080
91 hootatgaog taatttootig ggtgtgtgog ogogtgtgog tgogtgtgog tgtatataaa 1140
91 agonggoata goattgotgo tgotgongon gonanngona coatcanngo tgittancano 1800
93 acceptacting cartificate noting the acceptance and acceptate acceptance and acceptance acceptanc
94 obgecatoot ootgoagbag otogtobabt otttoogbab ogtooggoto gotatgego (1319)
97 K010 - SEQ ID NO: 6
98 K211 - LENGTH: 1760
99 KO125 TYPE: DNA
100 <213> OEGANISM: Mus musculus
102 <400> SEQUENCE: 6
103 gagaactite tetagetett teattagggg ceetgigtie catetaatag eigaeigiga 60
104 quatecactt etgtqcttdc daggcactgg datagectda daagagadag ctatatdagg 120
105 gtottgtdag daaaatotti otggdataig daatagigto igggittiggi ggittgtatai 180
106 gggetggate ecegggtggg geagtetetg gatggtettt cetteegtet tageteeaaa 240
107 offitgeofot graactooff coargogfac fftgfffccc affofaagaa ggagcaaagt 300
10% atecacactt cottottott pottottott gagttttgba aatgobacaa aactttbaaa 360
109 decttetgaa tageettete titagigett tecaaigtat attaaaataa tetaiettie 420
110 atococatty attacaged tertacaged agacagetat atteatttt ttettttede 480
111 agtagticae aaactateig geaecteata ageateataa eteagiiggi gggiagataa 540
111 dattggaatg tgattgttca gtcagcagag acttttagag gacctcatac aacaagattc 600
115 totoagttot cagaaatata titoagtata tacagggtta gaggactoac atotitaata 660
114 asataaadtt aaaaatttag acctgtataa attattaagg tacctaatca agttecacgg 720
115 caaagtacag ocatggttat gaattataaa tocaagaago ggtgggttaa ctotgacatt 780
116 gttocttgga tggttotoat toattgaagt tagtoacoto aacttactca accaaaacot 840
117 agaagtatti olgitggiaci algitolotti galigooaaga gggololagg calalgaaaa 900
110 aatocotooc ttootggtag goagtatgtt ttttggagsa cagtttotta gotatotott 1020
120 gcaacacetg attttgetga agatttgaat ggeeteatat agaagtatea acaacttgag 1080
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PATENT APPLICATION: US/09/804,409B TIME: 16:19:06

DATE: 06/25/2003

Input Set : A:\0278721.APP.txt

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1.1 ogtotgtgaa ototoatttt gadaetgtge tgaaagaatt ggagttgatt oteattaaaa 1140
1.2 aaaaaattaa goatotoaco tiittigoto aaactaaaca giittaaaac agiitoigoot 1200
113 ggagteatga tatgaaatae gatetateat atttgeaatg ttetgtteaa ttgtggetge 1160
114 accappaaat qaqaaqetat ttetttataq geacaaataa aaaqataqte attatetgta 1320
115 aaattottat gacatggcag caageecaag aaacetttet aaacaaggeg tgaaaacgca 1380
126 gagatgtoot tgoaattagt catgtotato tgacagattt ottootttot aagggaattt 1440
127 gtgotgaaca tittatitieg agesteagag ataaaaagaag ggggaagaag sigtagitit 1500
128 tyctacataa gacaggtggc gtaagcatgc aacgctttaa aaaaatatct aaagtgatty 1560
129 titteteteg gattetitga aaaagetege eigegeiggi gittgaggei gageeggiga 1620
130 ogtoagogtg gaatgoggag toaggogood aggetotota taagoogagg agetytoogg 1680
131 tgctgaaacg gcccgagccc tcactcagcg gcagagagga gcatgcttgg agccttccac 1740
13. ataatataag acagaggtaa
135 <110 / SEQ ID NO: 7
136 <011 · LENGTH: 2623
137 <212 - TYPE: DNA
13% <113 > ORGANISM: Mus musculus
140 <400 · SEQUENCE: 7
141 agotttaggt gtgtgaatat otaotttggt gotagggoot tggtbatact aagtaagttt 60
14% occettoact ggggtgtace agtttaceet ggaetgteta ageaacaaga aggatagaea 130
14% togeotacca cagatttoat gtotgecact ggotatgtoa gaacatgtag gagettttgg 140
144 aatcagtgaa acaggtatti toagactgoo ttoootgogt ggggotttoo ogaagocata 240
145 titttootag agtoagoott toocagotga ggacaagotg tactggacag atgocagoca 300
146 ettgaactgg gaatacatgg teatttagge agotggetta teteatoeat ggtaettgat 360
147 ggottogggt bagbabetba bagaaagtto agabgggagg bttbbggagaa aabagagaag 4.00
14% caqqeaqqaq atectqeaqq caatecteet getecasage etgeatggae tteecteage 480
149 ottaqtqoqt qtqqqtooca totqaqaaca ttqqttatat qttattttca aaccqatotq 540
150 ootttaagga gtggaagaaa aaaactgtgg tgtttgggot acctttatga taatggcott 600
15: ttoatootoo taataaatat tgocaagtag ggtagattot ataogaaago tottaacooa 660
152 tggtattage aaatcatgta ggtgetaata atgaatactg gatgeagtea gtacagggat 720
15) ataasatgga atgtaagago otgttgotat gaatggttag otaactagat gttgtacaag 760
154 aaatgttgad gttatgadgt gtggaaactt ggtattgaag atgtggadtd gaaactttgt 840
155 ggattttttg atgccatgat aaaaatgtga agaatactgt toottaccaa aaagaagaag 900
158 qaqqactaqq aqqaqqaqqa qaaqaaqqaq aagqqqaaqq agaqaqtaqc caqaacattt 10%0
159 ggggtgecat cagaatacea gatactecag acatagteac agaaggactg gtttgtttgt 1140
160 taaanaggig ettigaaaag tiigtgggga aaccigcagt gagatigigt giettagaaa 1200
101 tgataggdaa gattoatoba daagaatgog adaagatggo tgootgaada agoodtgaad 1160
10) attaacagea ccagtagaec tgettacaeg gaagaaagea ateteatagg coeteacece 1520
163 aaacaaagac tacagacago agaggaacty gagagcagga gaaattgggt otocotttta 1380.
184 tgaggeeest aastggttgt caaatastea atggtcages stgaaatsat atgcacaaag 1440
16\% taatastags gsaastgaas agattgtags tgtgtgtgtg tgtgtaatga taasaaagaa 1500
166 gaaaaggooc catgttagag agggagcaag gtgggcatgg aggtatggaa ggagttggaa 1560
167 ggagqggtga gaaggggaaa gtgatgtaat tatottttaa tttataaaaa aataaaaaat 1610
168 gggetggtga gatggeteag tgggtaagag bacoogaetg ettetteega aggtetggag 1680
169 ticaaatooc agcaaccaca tggtggotca caaccatcog taacgagato tggogoosto 1740
170 tictggagtg tetgaagaca getacagtgt acttacatat aataaataaa taaatetttt 1800
171 aaaaaaaata aaaaataaaa tattagaata aaatgtagag gaatattttt aatttaacaa 1~60
17. ontqqqtqtq qoaaaaqott tottoaacaa aaacttaato ootcagataa gaaaagacta 1920
```

PATENT APPLICATION: US/09/804,409B

DATE: 06/25/2003 TIME: 16:19:07

Input Set : A:\0278721.APP.txt

Output Set: N:\CRF4\06252003\I804409B.raw

173 qaatooacga ootooataga tacttotgta tgatgoaaga cactatttat caggitgtaa 1980 17% thachagata tittaqatga aabataanaa tactitocac aactgatagg taggaaacag 2000 17π ticaataqta atataattat igaacaauta atoottaaaa gaagaaatoo agaggaatag 1160177 calagitaggg galagagaggg tgtgtgtgtg tgtgtgtgcg cgcacattta tagocalaat 227017- agatgatata ottawatgaw batgobakta www.coatta tititgowtab wgtitwowia 22%0 17% tgotaatgaa taottaaaaa aaaaacaktg ggattggaga gasatggoto agtggttaag 2540 180 articaatie edagoaacea catgattyet cacaaceate igiaatggga toigatgeet 2400 1%1 tettetggta tgtetgaaga aagtgaeegt gtaettataa ttataaataa ataaatettt 24%018% asochaasaa oboccutaat tibaacauba gataiqibot ggibtgaggo tiboaggoat 25%018% Agalawtagaa acacacagag tgtggagcca gtgoggttca ggtoogcoat tocagttcag 1980164 gotthagaco aagagaaagg gaaaagawga gabaagcaac aag 187 - 110 - SEQ ID NO: 8 138 -711 - LENGTH: 226 189 - 211 - TYPE: DNA 190 -0215 - OEGANISM: Homo sapiens 19. - 400 - SEQUENCE: 8 14% thesegaaat degegationa geooggegig eggiglegigig getooggega gaggegigig 60%114 occurgatog deggegggeg gggegggagg eggggeegg eeegttaaga agagegtgge 1.00 14 -hygologogic calcegotype cocaggyala geogagege cacegageg geagagaeet 180146 accyagogyc ygoggagga gogacgongg ggogcacgag ggcacc 199 - 10 - SEQ ID NO: 9 200 - L11 - DENGTH: 110 201 - Wil. - TYPE: PRI 20. +115 * OFGANISM: Homo sapiens 304 - 400 - SEQUENCE: 9 1900 Met Ala Leu Trp Met Arq Leu Dau Pro Leu Leu Ala Leu Leu Ala Leu 10 10% Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Ash Gln His Leu Cys Gly 25 1000 311 Ser His Leu Val Glu Ala Leu Tvr Leu Val Cys Gly Glu Arg Gly Phe 35 40214 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly 5.5 50 117 Gln Val Glu Let Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu 75 219 65 70 this Ala Dec Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys 9:0 IL: Thr Jer Ile Cys Jer Leu Tyr Gin Leu Glu Asn Tyr Cys Asn 100105 110 117 HITE SEQ IP NO: 10 108 ×0110 LENGTH: 450 129 HILL TYPE: DNA .30 -011:00 OFGANISM: Homo sapiens 131 - 44000 SEQUENCE: 10 233 getycateag aagaggeeat caageacate actgteette tgecatggee etgtggatge 60° 244 gretection ectiotique etgetique tetgogram tataggame tyanomages graphettiq lab 1.% thateceases cotythologic tesesecting typesagetet etsectagity typiggyase 1.%256 gagyettett etacacaece aagadooyee gggaggeaga ggacetgeag gtggggeagg 240

PATENT APPLICATION: US/09/804,409B TIME: 16:19:07

DATE: 06/25/2003

Imput Set : A:\0278721.APP.txt

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237 taggagetagag cangagageset agatasagasa asestasagas ettagasseta gaagagatses 300
1138 tycayaaycy togcattyty gaacaatyct ytaccaycat ctyctocctc taccayctyy 360
239 agaactacty caactagacy cageoogeay yeagecoood accepteged teetgoacey 420
                                                                        450
1340 agagagatgg aataaagccc ttgaaccagc
243 <210> SEQ ID NO: 11
244 <211 · LENGTH: 167
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 11
249 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
                                          1.0
352 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
253
                 ()
                                      25
355 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
256
             35
                                  40
15% Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
                              55
261 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
                         70
164 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Ash Val Ile Gln
265
                     85
                                          90
167 Ile Ser Ash Asp Leu Glu Ash Leu Ard Asp Leu Leu His Val Leu Ala
268
                100
                                     105
070 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
            115
.:71
                                 120
                                                      125
273 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
      130
                             135
1:76 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
277 145
                        150
                                             155
079 Leu Asp Leu Ser Pro Gly Cys
280
183 <110> SEQ ID NO: 12
084 <011> LENGTH: 3408
285 <212> TYPE: DNA
086 <0135 ORGANISM: Homo sapiens
268 <400> SEQUENCE: 12
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290 ggattottgt ggotttggod statottttb tatgtocaag otgtgoccat ocaaaaagto 100
.341 cuagatgada domanaccot cateangada attigicacca ggatcaniga catticacae 140
191 acquaqtoaq totootocaa acaqaaaqto accqqtttqq acttoattoo tqqqotocac 240
{\mathbb C}{\mathbb W} occatoctga octiatocaa gatggaccag acactggcag totaccaaca gatoctcacc 300
124 agtatgeett ocaqaaaogt gatecaaata tooaaogabo tggagaacot oogggatett 3\pm 0
. 95 officacytige tygocticte taagayetye caettyceet gygocaytyy eetygayace 400
296 ttggabagbe tggggggtgt betggaaget tbaggbtabt beabagaggt ggtggbbbtg 480
197 ageaggetige aggggtetet geaggacatg etgtggeage tgjaceteag eeetgggtge 540
238 tgaggoettg aaggteacte tteetgeaag gactaegtta agggaaggaa etetggette 600
199 caggitatoto caggatigaa gagcatigoa iggacacoco tiatocagga cicigicaat 600
^{200} ticeetgast estetaages actetissaa aggeataaga eestaagest estittigett 7\%
501 gwaaccaaag atatatacac aggateetat teteaccagg aagggggtee acceagcaaa 780
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VERIFICATION SUMMARYDATE: 06/25/2003PATENT APPLICATION:US/09/804,409BTIME: 16:19:08

Input Set : A:\0278721.APP.txt